

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
- (B) STREET: 14 JOHN B. GROSIRAWEG
- (C) CITY: CURACAO
- (E) COUNTRY: NETHERLANDS ANTILLES
- (F) POSTAL CODE (ZIP): NONE
- (G) TELEPHONE: 639300
- (H) TELEFAX: 614129

(ii) TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTOTIC
CELL
DEATH PATHWAYS

(iii) NUMBER OF SEQUENCES: 6

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 206..616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGGCTGCTG TGGAGTTTGT GACATACTAG GTGACACCCT TGGAGTCACT TCTCTTCAAC
60

TCCAGCTTAG AAGTGCCTGC CTGGCTCAGG GTCTGCACTG CAGCCTACTC CTTGCTTCAG
120

GGCCTGACTG CAACGCCAAA GCCTATCCTA TAGCGGCAGC GCCAGCAGCC ACTCAAACCA
180

001120-1-1000000000

GCCACAGCTC CCCGGCAACC GAACC ATG AAC ACC GAA ATG TAT CAG ACC CCC
232

Met Asn Thr Glu Met Tyr Gln Thr Pro
1 5

ATG GAG GTG GCG GTC TAT CAG CTG CAC AAT TTC TCC ACC TCC TTC TTT
280

Met Glu Val Ala Val Tyr Gln Leu His Asn Phe Ser Thr Ser Phe Phe
10 15 20 25

TCT TCT CTG CTT GGA GGG GAT GTG GTT TCC GTT AAA CTG GAT AAC AGT
328

Ser Ser Leu Leu Gly Gly Asp Val Val Ser Val Lys Leu Asp Asn Ser
30 35 40

GCC TCC GGA GCC AGT GTG GTG GCC CTA GAC AAC AAG ATT GAG CAG GCC
376

Ala Ser Gly Ala Ser Val Val Ala Leu Asp Asn Lys Ile Glu Gln Ala
45 50 55

ATG GAC CTC GTG AAG AAC CAC CTG ATG TAC GCT GTG AGA GAG GAG GTG
424

Met Asp Leu Val Lys Asn His Leu Met Tyr Ala Val Arg Glu Glu Val
60 65 70

GAG GTC CTA AAG GAG CAG ATT CGT GAG CTG CTT GAG AAG AAC TCC CAG
472

Glu Val Leu Lys Glu Gln Ile Arg Glu Leu Leu Glu Lys Asn Ser Gln
75 80 85

CTG GAG CGC GAG AAC ACC CTC CTG AAG ACG CTG GCA AGC CCC GAG CAA
520

Leu Glu Arg Glu Asn Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln
90 95 100 105

CTG GAA AAG TTC CAG TCC CGG CTG AGC CCT GAA GAG CCA GCA CCT GAA
568

Leu Glu Lys Phe Gln Ser Arg Leu Ser Pro Glu Glu Pro Ala Pro Glu
110 115 120

GCC CCA GAA ACC CCG GAA ACC CCG GAA GCC CCT GGT GGT TCT GCG GTG
616

Ala Pro Glu Thr Pro Glu Thr Pro Glu Ala Pro Gly Gly Ser Ala Val
125 130 135

TAAGTGGCTC TGTCCCTTAGG GTGGGCAGAG CCACATCTTG TTCTACCTAG TTCTTTCCAG
676

TTTGTTTTTG GCTCCCCAAG GGTCATCTCA TGTGGAGAAC TTTACACCTA ACATAGCTGG
736

TGCCAAGAGA TGTCCCAAGG ACATGCCCAT CTGGGTCCAC TCCAGTGACA GACCCCTGAC
796

AAAGAGCAGG TCTCTGGAGA CTAAGTTGCA TGGGGCCTAG TAACACCAAG CCAGTGAGCC
856

TGTCGTGTCA CCGGGCCCTG GGGGCTCCCA GGGCTGGGCA ACTTAGTTAC AGCTGACCAA
916

09403864.021100

GGAGAAAGTA GTTTTGAGAT GTGATGCCAG TGTGCTCCAG AAAGTGTAAG GGGTCTGTTT
976

TTCATTTCCA TGGACATCTT CCACAGCTTC ACCTGACAAT GACTGTTCCCT ATGAAGAAGC
1036

CACTTGTGTT CTAAGCAGAA GCAACCTCTC TCTTCTTCCT CTGTCTTTTC CAGGCAGGGG
1096

CAGAGATGGG AGAGATTGAG CCAAATGAGC CTTCTGTTGG TTAATACTGT ATAATGCATG
1156

GCTTTGTGCA CAGCCCAGTG TGGGGTTACA GCTTTGGGAT GACTGCTTAT AAAGTTCTGT
1216

TTGGTTAGTA TTGGCATCGT TTTTCTATAT AGCCATAATG CGTATATATA CCCATAGGGC
1276

TAGATCTATA TCTTAGGGTA GTGATGTATA CATATACACA TACACCTACA TGTTGAAGGG
1336

CCTAACCAGC TTTGGGAGTA CTGACTGGTC TCTTATCTCT TAAAGCTAAG TTTTGGACTG
1396

TGCTAATTTA CCAAATTGAT CCAGTTTGTC CTTTAGATTA AATAAGACTC GATATGAGGG
1456

AGGGAGGGGA AGACCAGCCT CACAATGCGG CCACAGATGC CTTGCTGCTG CAGTCCTCCC
1516

TGATCTGTCC ACTGAAGACA TGAAGTCCTC TTTTGAATGC CAAACCCACC ATTCATTGGT
1576

GCTGACTACA TAGAATGGGG TTGAGAGAAG ATCAGTTTGG ACTTCACATT TTTGTTTTAA
1636

GTTTGTAGTT GTTTTTTTTT GGTTTTGTTT GTTTGTTTGT TTGTTTGTTT TTGTTTTTTG
1696

TTTTTCTTTT TTAAGTTCTT GTGGGGAAAC TTTGGGGTTA ATCAAAGGAT GTAGTCCTGT
1756

GGTAGACCAG AGGAGTAACT AGTTTTGATC CTTTGGGGTG TGGAAAATGT ACCCAGGAAG
1816

CTTGTGTAAG GAGGTTCTGT GACAGTGAAC ACTTCCACT TTCTGACACC TCATCCTGCT
1876

GTACGACTCC AGGATTGGA TTTGGATTTT TCAAATGTAG CTTGAAATTT CAATAAACTT
1936

TGCTCCTTTT TCTAAAAATA AAAAAAAAAA AAAAAA
1972

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln
1 5 10 15
Leu His Asn Phe Ser Thr Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp
20 25 30
Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val
35 40 45
Ala Leu Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His
50 55 60
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln Ile
65 70 75 80
Arg Glu Leu Leu Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu
85 90 95
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Arg
100 105 110
Leu Ser Pro Glu Glu Pro Ala Pro Glu Ala Pro Glu Thr Pro Glu Thr
115 120 125
Pro Glu Ala Pro Gly Gly Ser Ala Val
130 135

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "PCR forward primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCATCTGGGT CCACTCCAGT
20

001120-1980460

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /note= "PCR reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AGGACAGTGG GAGTGGCACC
20

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1946 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 241..642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AATTCGGGGG CCGTGGAGTT TGTGACATAC GAGGTGACAC CCCTCGAGTC ACTTCCCTTC
60

AACTCCAGCT GGAGCGCCTG CTTGGCTTTG GGTTCGTTCT GCAGCCTTCG CCCCCTCCTC
120

AGCCTCAGGG CCGGACTCCA GCGCAGAGCC CAGCCCAGCG CAGCCTGCCA GCAGCCACCC
180

AGCCGCCCAG CCGCCCAGCC CCGCACGAAA CCCGGCCAGA GCTTCCTAGC AGCCCGAGCC
240

001120113300460

ATG AAC ACC GAA ATG TAT CAG ACC CCC ATG GAG GTG GCG GTC TAC CAG
288
Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln
5 10 15

CTG CAC AAT TTC TCC ATC TCC TTC TTC TCT TCT CTG CTT GGA GGG GAT
336
Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp
20 25 30

GTG GTT TCC GTT AAG CTG GAC AAC AGT GCC TCC GGA GCC AGC GTG GTG
384
Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val
35 40 45

GCC ATA GAC AAC AAG ATC GAA CAG GCC ATG GAT CTG GTG AAG AAT CAT
432
Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His
50 55 60

CTG ATG TAT GCT GTG AGA GAG GAG GTG GAG ATC CTG AAG GAG CAG ATC
480
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile
65 70 75 80

CGA GAG CTG GTG GAG AAG AAC TCC CAG CTA GAG CGT GAG AAC ACC CTG
528
Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu
85 90 95

TTG AAG ACC CTG GCA AGC CCA GAG CAG CTG GAG AAG TTC CAG TCC TGT
576
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys
100 105 110

CTG AGC CCT GAA GAG CCA GCT CCC GAA TCC CCA CAA GTG CCC GAG GCC
624
Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala
115 120 125

CCT GGT GGT TCT GCG GTG TAAGTGGCTC TGTCCTCAGG GTGGGCAGAG
672
Pro Gly Gly Ser Ala Val
130

CCACTAACT TGTTTTACCT AGTTCTTTCC AGTTTGTTTT TGGCTCCCCA AGCATCATCT
732

CACGAGGAGA ACTTTACACC TAGCACAGCT GGTGCCAAGA GATGTCCTAA GGACATGGCC
792

ACCTGGGTCC ACTCCAGCGA CAGACCCCTG ACAAGAGCAG GTCTCTGGAG GCTGAGTTGC
852

ATGGGGCCTA GTAACACCAA GCCAGTGAGC CTCTAATGCT ACTGCGCCCT GGGGGCTCCC
912

AGGGCCTGGG CAACTTAGCT GCAACTGGCA AAGGAGAAGG GTAGTTTGAG GTGTGACACC
972

00403861 021100

AGTTTGCTCC AGAAAGTTTA AGGGGTCTGT TTCTCATCTC CATGGACATC TTCAACAGCT
1032

TCACCTGACA ACGACTGTTT CTATGAAGAA GCCACTTGTG TTTTAAGCAG AGGCAACCTC
1092

TCTCTTCTCC TCTGTTTCGT GAAGGCAGGG GACACAGATG GGAGAGATTG AGCCAAGTCA
1152

GCCTTCTGTT GGTAAATATG GTATAATGCA TGGCTTTGTG CACAGCCCAG TGTGGGATTA
1212

CAGCTTTGGG ATGACCGCTT ACAAAGTTCT GTTTGGTTAG TATTGGCATA GTTTTTCTAT
1272

ATAGCCATAA ATGCGTATAT ATACCCATAG GGCTAGATCT GTATCTTAGT GTAGCGATGT
1332

ATACATATAC ACATCCACCT ACATGTTGAA GGGCCTAACC AGCCTTGGA GTATTGACTG
1392

GTCCCTTACC TCTTATGGCT AAGTCTTTGA CTGTGTTTAT TTACCAAGTT GACCCAGTTT
1452

GTCTTTTAGG TTAAGTAAGA ACTCGAGAGT AAAGGCAAGG AGGGGGGCCA GCCTCTGAAT
1512

GCGGCCACGG ATGCCTTGCT GCTGCAACCC TTTCCCCAGC TGTCCACTGA AACGTGAAGT
1572

CCTGTTTTGA ATGCCAAACC CACCATTAC TGGTGCTGAC TACATAGAAT GGGTTGAGAG
1632

AAGATCAGTT TGGGCTTCAC AGTGTCATTT GAAAAAGCGT TTTTGTTTTG TTTTGAATTA
1692

TTGTGGAAAA CTTTCAAGTG AACAGAAGGA TGGTGTCCTA CTGTGGATGA GGGATGAACA
1752

AGGGGATGGC TTTGATCCAA TGGAGCCTGG GAGGTGTGCC CAGAAAGCTT GTCTGTAGCG
1812

GGTTTTGTGA GAGTGAACAC TTTCCACTTT TTGACACCTT ATCCTGATGT ATGGTTCCAG
1872

GATTTGGATT TTGATTTTCC AAATGTAGCT TGAAATTTCATAAACTTTG CTCTGTTTTT
1932

CTAAAAAATA AAAA
1946

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln
1 5 10 15
Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp
20 25 30
Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val
35 40 45
Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His
50 55 60
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile
65 70 75 80
Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu
85 90 95
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys
100 105 110
Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala
115 120 125
Pro Gly Gly Ser Ala Val
130

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